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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2996.72 Seconds  
(without alignments)  
11304.265 Million cell updates/sec

Title: US-09-807-933B-10  
Perfect score: 1164  
Sequence: 1 atgaagtccacgttgctat.....cagggtgcgaagaagtaa 1164

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
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7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
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12: gb.sy.\*  
13: gb.un.\*  
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40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	251.6	21.6	840	3	AB045172	AB045172 Reticulic
2	246.8	21.2	828	3	AB045179	AB045179 Reticulic
3	244.2	21.0	730	3	AB045168	AB045168 Reticulic
4	241.8	20.8	808	3	AB045178	AB045178 Reticulic
5	240.6	20.7	710	3	AB045171	AB045171 Reticulic
6	233.4	20.1	774	3	AB045170	AB045170 Reticulic
7	232.8	20.0	781	3	AB045165	AB045165 Reticulic
8	231	19.8	784	3	AB045167	AB045167 Reticulic
9	227.8	19.6	798	3	AB045166	AB045166 Reticulic
10	221.4	19.0	1443	8	FSOKCH	L29381 Fusarium ox
11	221.4	19.0	1473	6	A21795	A21795 F. oxysporum
12	221.4	19.0	1473	6	A23637	A23637 F. oxysporu
13	221.4	19.0	1473	6	A23646	A23646 F. oxysporu
14	221.4	19.0	1473	6	A23955	A23955 Endoglucana
15	221.4	19.0	1473	6	A23959	A23959 Endoglucana
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17	221.4	19.0	1473	6	AR072922	AR072922 Sequence
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19	221.4	19.0	1473	6	BD010853	BD010853 Cellulase
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22	221.4	19.0	1473	6	I57984	I57984 Sequence 3
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24	213.6	18.4	785	3	AB045169	AB045169 Reticulic
25	212.2	18.2	759	3	AB045174	AB045174 Reticulic
26	212.2	18.2	802	3	AB045176	AB045176 Reticulic
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31	204	17.5	912	6	AR163170	AR163170 Sequence
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33	202.8	17.4	919	6	AR163168	AR163168 Sequence
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35	200.6	17.2	924	6	AR163169	AR163169 Sequence
36	188	16.2	922	6	A68078	A68078 Sequence 73
37	188	16.2	922	6	AR163171	AR163171 Sequence
38	186.8	16.0	922	6	A68070	A68070 Sequence 65
39	186.8	16.0	922	6	AR163167	AR163167 Sequence
40	186	16.0	1154	6	AR094308	AR094308 Sequence
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ALIGNMENTS

RESULT 1  
AB045172  
LOCUS  
DEFINITION  
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:8-44, complete cds.  
ACCESSION  
AB045172  
VERSION  
AB045172.1  
KEYWORDS  
GI:5926976  
SOURCE  
Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA, clone:8-44.  
ORGANISM  
Reticulitermes speratus hindgut symbiont 130484  
Unclassified.  
REFERENCE  
1 (sites)  
AUTHORS  
Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.  
TITLE  
Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite  
Reticulitermes speratus  
Extremophiles 4 (6), 343-349 (2000)  
21020023  
2 (bases 1 to 840)  
Ohkuma, M.  
Direct Submission  
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of  
Physical and Chemical Research), Microbiology Laboratory; Hirose  
2-1, Wako-shi, Saitama 351-0198, Japan  
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,  
Fax:66-48-462-4672)  
Location/Qualifiers  
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BASE COUNT 227 a 157 c 200 g 256 t  
ORIGIN

Query Match 21.6%; Score 251.6; DB 3; Length 840;  
Best Local Similarity 65.4%; Pred. No. 3e-55;  
Matches 403; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

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DB 78 TGGGAGGACCAACCGCTTACTGGAGCTGTGCAAGAGCTTCGTGTGCATGGGAAAAAAGC 137

QY 615 TTCTGTCACTGTCTGTGTGACACCTGTGCCTCCAAATGGTATCTTTATTAG-----A 668  
DB 138 TCGTGTGACTAGCTGTGTGACACATGGCGAAAGATGGCAACACAGAGTGTGAAGCAA 197

QY 669 TCCCAATGCTCAAGTGGTGTGTAACCGTGGTAAATGGTTTCAATGTGTAACAACCAACCA 728  
DB 198 TGACACAGTGAATCTTGTGTGTGATGGAGAGGATACATGTGTATGATCAAGCACC 257

QY 729 TTGGGCTGTCAATGATGAGCTCGTTACGGTTTCGCTTCTGCTTATTTGGCTCCAA 788  
DB 258 TTGGGCTGTAAATGACTCGGTGTGCATACGGTTTTCGGCTGCGAGCTTGTCTGTGG---AGG 314

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DB 315 CGAAGCGGTGTGTGTGCAATGTGTATGAGCTTACCTTCCAGTGGCCAGTTAATGG 374

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QY 909 TTTGCAATCCCGGTGGTGGCGTGTGTATCTTCAATGGCTGTGTCTCAATGGGCGC 968  
DB 435 TCTTGCATTTCCCGGAGGAGTGTCCGAAATTACATGGATGCACTCAACAATCAGGGGC 494

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QY 1029 TCTTCCCTCTGCTTCTCAAGCTGTGTGTAATGGAGATTCAACTGGTTTCAAGAACTCTGA 1088  
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DB 615 CAACCCITCAATCAATTTCAATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 674

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DB 675 TTGCAAGCGAAGCTAA 690

RESULT 2  
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LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45  
DEFINITION cellulase homologue, clone:6-47, complete cds.  
ACCESSION AB045179  
VERSION AB045179.1 GI:8926990  
KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,  
SOURCE Reticulitermes speratus hindgut symbiont 130484  
ORGANISM Reticulitermes speratus hindgut symbiont 130484  
UNCLASSIFIED.  
REFERENCE 1 (sites)  
AUTHORS Ohkuma, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.  
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family  
45 from the symbiotic protists in the hindgut of the termite  
Reticulitermes speratus  
Extremophiles 4 (6), 343-349 (2000)  
MEDLINE 21020023  
REFERENCE 2 (bases 1 to 828)  
AUTHORS Ohkuma, M.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of  
Physical and Chemical Research), Microbiology Laboratory; Hirose  
2-1, Wako-shi, Saitama 351-0198, Japan  
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,  
Fax:66-48-462-4672)  
Location/Qualifiers  
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BASE COUNT 231 a 133 c 208 g 256 t  
ORIGIN

Query Match 21.2%; Score 246.8; DB 3; Length 828;  
Best Local Similarity 64.9%; Pred. No. 5.5e-54;  
Matches 400; Conservative 0; Mismatches 207; Indels 9; Gaps 2;

QY 555 TGGTTCACCAACTCGTTATGGAGTGTGTAAGCTTCTTGCAGCTGGCGCTGGAAAGC 614  
DB 79 TGGGAGGACTACGCTTATTTGGAGTGTGTCGAAAGCGTTCATGTGCAATGGAAAGC 138

QY 615 TTCTGTCACTGGTTCCTGTGACACCTGTGCCTCCAAATGGTATCTCTTTATTAG-----A 668  
DB 139 TGCTGTGACTCAGCTTGTGATAGCTGTGGAAGATGGGACAAAGACTTGCAGACAA 198

QY 669 TGCCAAATGCTCAAGTGGTGTGTAACGGTGGTAAATGGTTTCACTGTGTAACAACCAACCA 728  
DB 199 TGACACAGTAAATCGAGTTGTGATGCGGAGATGGATACATGTGTATGATCAAGCACC 258

QY 729 TTGGCTGTCAATGATGAGCTCGCTTACGGTTTTCGCTGTGCTCTATTCTGCTGCTCCAA 788  
DB 259 ATGGGCTGTAAATGACTCAGTTGCTATGTTTGGAGCTGCAGCTTGTGTGG---AGG 315

QY 789 CGAAGCTGGATGGTGTGTGGCTGTATGAAATGACCTTCACTTCTGCGCTGCTTCTG 848

Db 316 TGAGACTGGAGCTTGTTCGAATTCTATGAGCTTAAGCTTACAGAGTGGCCAGTGAATGG 375

QY 849 AAGAAGATGGTGTTCGAAGTTACCAACACCGGTGGCGATTATAGGCTCTAAACACATTTGA 908

Db 376 AAGAAGATGGTGTTCGAAGTTACCAACACCGGTGGCGATTATAGGCTCTAAACACATTTGA 435

QY 909 TTTGCAAAATGCCCGGTGGTGGCTTGTGATCTTCAATGGCTGTGCTCAATGGGGCGC 968

Db 436 TCTTGCAAATTCACAGGAGGAGTGTGGAATTTACAATGGATGCACTCAGCAATCAGGTGC 495

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Db 616 CAACCTTCAATCAATTTCAACCAAGTACATGCCCAAGTGAATTTGATAGCAAGAACCA 675

QY 1149 TTGCGAAGAAAGTAA 1164

Db 676 TTGCAAAACGTACTTAA 691

RESULT 3

AB045168 780 bp mRNA linear INV 14-FEB-2001

LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

DEFINITION cellulase homologue, clone:4-44, complete cds.

ACCESSION AB045168

VERSION AB045168.1 GI:8926968

KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cdna to mRNA, clone:4-44.

SOURCE Reticulitermes speratus hindgut symbiont 130484

ORGANISM Unclassified.

REFERENCE 1 (sites)

AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.

TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus

JOURNAL Extremophiles 4 (6), 343-349 (2000)

MEDLINE 2102023

REFERENCE 2 (bases 1 to 780)

AUTHORS Ohkuma,M.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosewa 2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES

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BASE COUNT 196 a 155 c 206 g 223 t

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Query Match 21.0%; Score 244.2; DB 3; Length 780;

Best Local Similarity 64.4%; Pred. No. 2.6e-53;

Matches 401; Conservative 0; Mismatches 213; Indels 9; Gaps 2;

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Db 64 TGTGACAGTGTGGCAAAACGACCCGCTATTGGGACTGCTGCAAAAGGCTCTCTGTGGCTGGAA 123

QY 607 GGAAAGAGTTTGTCACTGGTCTCTGTGACACCTGTGCTCCAATGGTATCTCTTTATTAA 666

Db 124 GCCAAAGCTGATGTTCAGCAAAACCGATAGACACGTGCGCAAAAGATGGCACAACTCGAGTT 183

QY 667 GATGCCAATGCTC-----AAAGTGGTTGTAACGGTGGTAATGGTTTCAATGTGTACAAC 720

Db 184 GCAAGCAACGATACAGTAAATCTGTTGTGTATGGCGGTGACGGGCTTCAATGTGCTACGAT 243

QY 721 AACCAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCTCTATTGCT 780

Db 244 CAACCCCGTGGGGGTCAACGATTTCTTACGGTTGGGATTTGCTGCTCAGCAATTTCA 303

QY 781 GGCTCCAAACGAAGCTGGATGGTGTGTGGCTGTATGAAATTGACCTTCACTTCTGGCGCT 840

Db 304 GGAGGTGAGAA-3GCTGCCCTGCTGTAAT---TGTACGAGTTGACTTTCACTCTGSCCCC 360

QY 841 GCTTCTGGAAGAAGATGGTTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAAC 900

Db 361 GTTAATGGCAAGAAGATGACTCTTCAGGTTTACCAACACCGGAGGTGATCTCGGTTGCAAT 420

QY 901 CACTTTGATTTCGCAATGCCCGTGGTGGTGTATCTTCAATGGGCTGCTGCTCAA 960

Db 421 CAATTTGATCTCGCCATTCAGGTGGTGGTGTGCGGTATTATCAATGGATGCAACAGCTCAA 480

QY 961 TGGGGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTGTCAGCTCTGTCTGAC 1020

Db 481 TCTGGTGTCTCTGCTGCTTGGGGAAGTCGCTATGGAGGGGTCTCTCTCCCGCAGTGAA 540

QY 1021 TGTGCTCTCTTCCCTCTGCTCTTCAAGCTGGTGTGTAATGAGATTAACCTGTTTCAAG 1080

Db 541 TGTCTCCAGCTTCTTCTGGGGTCTTCAGGCTGCTGCCAGTGGAGATTCGATTTGGTTCCAA 600

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QY 1141 CGCTCAGGTTTGCFAAAGAAAGTA 1163

Db 661 AAAACCAATTGCAGCGCAATTA 683

RESULT 4

AB045178 808 bp mRNA linear INV 14-FEB-2001

LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

DEFINITION cellulase homologue, clone:45-6, complete cds.

ACCESSION AB045178

VERSION AB045178.1 GI:8926988

KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cdna to mRNA, clone:45-6

SOURCE Reticulitermes speratus hindgut symbiont 130484

ORGANISM Unclassified.

REFERENCE 1 (sites)

AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.

TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus

JOURNAL Extremophiles 4 (6), 343-349 (2000)

MEDLINE 2102023

REFERENCE 2 (bases 1 to 808)

AUTHORS Ohkuma,M.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosewa 2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,

FEATURES  
source

AB045171.1 GI:8926974  
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,  
clone:7-50.  
Reticulitermes speratus hindgut symbiont 130484  
Unclassified.

ORGANISM  
1 (sites)  
Ohtoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.  
Diverse genes of cellulase homologues of glycosyl hydrolase family  
45 from the symbiotic protists in the hindgut of the termite  
Reticulitermes speratus  
Extremophiles 4 (6), 343-349 (2000)  
21020023  
2 (bases 1 to 710)  
Ohkuma, M.  
Direct Submission  
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of  
Physical and Chemical Research), Microbiology Laboratory, Hirosewa  
2-1, Wako-shi, Saitama 351-0198, Japan  
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,  
Fax:66-48-462-4672)

REFERENCE  
TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
JOURNAL

FEATURES  
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BASE COUNT 185 a 137 c 197 g 191 t

ORIGIN

Query Match 20.7%; Score 240.6; DB 3; Length 710;  
Best Local Similarity 64.1%; Pred. No. 2.3e-52;  
Matches 398; Conservative 0; Mismatches 214; Indels 9; Gaps 2;

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DB 419 TTTGATCTTGGGATTCGGGCTGGAGTGTGGGATCTACCAACCGGTGGACCCAGCAATCA 478  
QY 964 GGCGCTCCCAATGANGGCTGGGGAGCTAGATATGGTGGTGTCTGCTGCTGCTGCTGCT 1023

RESULT 5  
AB045171  
LOCUS  
DEFINITION  
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45  
cellulase homologue, clone:7-50, complete cds.



us-09-807-933b-10.rge

Wed Jun 18 17:54:54 2003

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BASE COUNT 193 a, 143 c 210 g 235 t

ORIGIN

Query Match 20.0%; Score 232.8; DB 3; Length 781;  
Best Local Similarity 63.4%; Pred. No. 2.7e-50;  
Matches 392; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

553 AGTGGTTCACAACTCGTTATTGGGATTTGTTAAAGCTTCTTGACGCTGCGCTGGAAGA 612  
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73 AGTGGCAGAACACCCGCTACTGGATTCGTCMAAGGAAGTTGGGTGGAGCAAG 132  
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613 GTTCTGTCTACTGCTGCTGTTGACCTGCTCCCAATGGTATCTCTTTATTAG----- 667  
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133 GCTGATGTAGCAAGCACTATTGTATACATGTCGAGAGATGGCACAAGAGTTGCAAGT 192  
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668 -ATGCCAATGCTCAAGTGGTTGTAACGGTGGTAATGGTTTCTATGTGTAAACAACCAA 726  
|||||  
193 AACGATACGGTTAATCCGGCTGTGATGGTGGAGAAGATACATGTTTATGATCAACG 252  
|||||  
727 CTTGGGCTGTCAATGATGACCTCGCTTACGTTTCTGCTGCTCTCTATTGCTGCTCC 786  
|||||  
253 CCTCGTGTCTCAATGATCTTATGCAATTTGGCTTCGCGCTGCGGCTATCTCAGGAGGA 312  
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787 AACGAAGCTGGATGCTGTTGGCTGTTGATGAATGACCTTCACTTCTGCGCTGCTTCT 846  
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313 GAGAGGCTG-----CTTGTGCGAGTGTACGAATTTGACTTTTCACTCGGACCGGTGAT 369  
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847 GGAAGAAGATGGTTGTTCAAGTTTACCAACACCGGTGGCGATTTAGGCTCTAACCACTTT 906  
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370 GGAAGAAGATGACTGTTTCAAGTTTACTAACACTGGGGCGATCTTGGTTCCAACCACTTT 429  
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907 GATTTCGAATGCGCGGTGGTGGTGTATCTTCAATGCTGCTGCTGCTCAATGGGC 966  
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430 GATCTTGTATTCTCAGGGGTGGTGGGAATATATATGATGATGACCGCTCAATCTGTT 489  
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967 GCTCCCAATGATGCTGGGAGCTAGATATGTTGGTGTGACGCTCTGCTGCTGCTGCTG 1026  
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490 GCTCCTGATGATGGAGGACCGATATGGCGGTGTTTCTCTCGTAGTGAATGTTCC 549  
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1027 TCTCTTCTCTGCTCTTCAAGTGTGTTAAATGGAGATTCACCTGTTTCAAGACTCT 1086  
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550 CAGCTTCAATCAGCTCTCAGGCTGGATGCGAGTGGCGATTTGATTTTCCAAATGCA 609  
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670 AATTGCAGACGTAATTA 687  
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RESULT 8  
AB045167 784 bp mRNA linear INV 14-FEB-2001  
LOCUS  
DEFINITION  
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45  
cellulase homologue, clone:8-16, complete cds.

ACCESSION  
AB045167  
AB045167.1 GI:8926966

VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,  
clone:8-16.  
Reticulitermes speratus hindgut symbiont 130484  
Unclassified.

REFERENCE  
1 (site)  
Ohtoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.  
Diverse genes of cellulase homologues of glycosyl hydrolase family  
45 from the symbiotic protists in the hindgut of the termite  
Reticulitermes speratus  
Extremophiles 4 (6), 343-349 (2000)

JOURNAL  
MEDLINE  
21020023

2 (bases 1 to 784)  
Ohkuma, M.  
Direct Submission  
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of  
Physical and Chemical Research), Microbiology Laboratory, Hiroseawa  
2-1, Wako-shi, Saitama 351-0198, Japan  
(E-mail:mohkuma@malman.riken.go.jp, Tel:66-48-467-9545,  
Fax:66-48-462-4672)  
Location/Qualifiers  
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RN"

BASE COUNT 202 a 153 c 210 g 219 t

ORIGIN

Query Match 19.8%; Score 231; DB 3; Length 784;  
Best Local Similarity 63.1%; Pred. No. 7.9e-50;  
Matches 392; Conservative 0; Mismatches 220; Indels 9; Gaps 2;

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609 AAAGCTTCTCTACTGCTGCTGTGACACTGCTGCCATCGCTCAATGGTATCTTTATTAG- 667  
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132 AAAGCCCATGTTAGCAAGCCCATTGACATGCGCGAAAGATGGGACCAACAGAGTTGC 191  
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668 -----ATGCCAATGCTCAAGTGGTGTGACGCTGGTAAATGGTTTCAATGTGTAACAACA 722  
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192 AAGCAACGACACCGGTGAAAGTGGTTGTATGTCGGGGAGCGGATACATGTGCTATGATCA 251  
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723 CCACCTTGGGCTGTCATATGATGAGCTGCTTACGCTTACGCTGCTGCTCTTATGCTGG 782  
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252 AACACCGTGGGCTGTTATGATTCATATGCCCTTGGCTTTCGCTGCTGCGCAATTT CAGG 311  
|||||  
783 CTCCAAAGAGCTGATGGTGTGCTGCTGTTATGATGATGACCTTCACTTCTGCGCTGC 842  
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312 AGCGAAAGAGCGCGCA---TGCTGCAACTGTTTACGAACTTACGTTCACTCTGCGCCGT 368  
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843 TTCTGGAAGAGATGGTTGTTTCAAGTTACCAACACCGGTGGCGGATTTAGGCTCTAACCA 902  
|||||  
369 CAATGGCAAGAGATGACTGTGCGAGTTACCAACACTGGAGGCGACTTGGGTTCACCA 428  
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903 CTTTGAATTCGAAATGCCCGGTGGTGGCTGTTGATCTTCAATGCTGCTGCTCAATG 962  
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429 ATTGATCTTGCATACCTGCTGGCGAGTGGGAATTTATATGATGACACAGCTCAGTC 488  
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963 GGGCGCTCCCAATGATGCTGGGAGCTAGATATGTTGGTGTGACGCTGCTGCTGCTGCTG 1022  
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489 TGGTCTCTCTCCGATGGGTGGGAGTGGTATGAGGGGTTTCTCTCGCAGCGGAATG 548  
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549 CTCCTCAACTCTCTTTCAGGCTCTTCAAGCTGGCTGCGAGTGGAGATTTGATTTGTTCCAAA 608  
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1083 CTCCTGATAACCTTACCAGCTTCAAGGAGGTTTACCTGCTGCTGCTGCTGCTGCTGCTG 1142  
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609 TCCCGACCAATTCGTTCCATGAACTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668  
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1143 CTCAGGTTTCGGAAGAAAGTA 1163  
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669 AACCAATTGCAGACGCAATTA 689  
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RESULT 9
AB045166
LOCUS
DEFINITION
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:2-6, complete cds.
ACCESSION
AB045166
VERSION
AB045166.1 GI:8926964
KEYWORDS
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
Clone:2-6.
SOURCE
Reticulitermes speratus hindgut symbiont 130484
Unclassified.
ORGANISM
Ohtoko.K., Ohkuma.M., Moriya.S., Inoue.T., Ueami.R. and Kudo.T.
Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
2102023
REFERENCE
2 (bases 1 to 798)
Ohkuma.M.
Direct Submission
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirotsawa
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)
FEATURES
Location/Qualifiers
1..798
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/clone="2-6"
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RN"
BASE COUNT 195 a 154 c 226 g 222 t 1 others
ORIGIN
Query Match 19.6%; Score 227.8; DB 3; Length 798;
Best Local Similarity 62.8%; Pred. No. 5.5e-49;
Matches 390; Conservative 0; Mismatches 222; Indels 9; Gaps 2;
QY 549 TGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAGCTTCTTGCAGCTGGCGCTCG 608
DB 74 TGACATGGGCAAAACAAACAAAGGATTGGGACTCTGCAAGGCGAGTTGTGGCTGGGAAGC 133
QY 609 AAAAGCTTCTGTCACTGGTCTCTGTGACACCTGTGCTCCAATGGTATCTCTTTATTAG- 667
DB 134 GAAAGCGGAGCTGAGCAAGCCATTGCACATGCGCGAAGACGGGACCAACAGAGTTGC 193
QY 668 -----ATGCCAATGCTCAAAGTGGTTGTAACGGTGTATGTTTCATGTGTAACAACAA 722
DB 194 GAGCAACGACACCGTGAAGAGTGGTTGTGATGCGGGGACGGTTATATGTGCTATGATCA 253
QY 723 CCAACCTTGGGCTGCAATGATGAGCTCGCTTACGCTTTCGCTGCTGCTCTATTGCTGG 782
DB 254 AACACGTTGGGGGTCAACGACTCATACGCCCTTGGGCTTGTGCTGCGACCAATTCAGG 313
QY 783 CTCACACGAGCTGGATGGTTGTGGCTGTTATGAATGACCTTCACTTCTGGGCGCTGC 842
DB 314 CGCGGAGAGGCTG---CTTGCTGCAACTGTTATGATTTGACATTCATCTTCTGGCCCGT 370
QY 843 TTCTGGAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGAATTAGGCTCTTAACCA 902

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371 TAATGGCAAGAAGATGACAGTACAGGTTACCAACACATGGAGGCGAGCTTGGTGTCCAATCA 430
QY 903 CTTTTCATTTGCAAAATGCCCGTGGTGGCTATCTTCAATGGCTGTGCTCTCAATG 962
DB 431 ATTTCATCTTGAATTCAGGCGGGTGTGGGCACTCTACAATGATGACGCGCTCAGTC 490
QY 963 GGGCGCTCCCAATATGGCTGGGAGCTAGATATATGGTGTGTCAGCTCTGTCTCTGACTG 1022
DB 491 TGGCGCTCTCTGCTGACGGATGGGTAGTCGGTATGGTGAGTTTCTCTCGCAGCAATG 550
QY 1023 TGCTCTCTCTCTCTCTCTCTTCAAGCTGGTGTGAAATGGAGATTCACATGGTTCAAGAA 1082
DB 551 CTCGCAACTTCTTTCAGGCTCTTTCAGGCTGGCTGCCAGTGGAGATTGATTGGTTCAAAA 610
QY 1083 CTCTGATAACCCCTACATGACCTTCAAGGAGCTTACCTGCTCTCTGCTGAATTAACACTACTCG 1142
DB 611 CGCCGACATCTCGTCTCAATGATTCATATGTTGGTGTGCTGCCCCAGTGAGTTGATTCGGA 670
QY 1143 CTCAGGTTTGGCAAGAAAGTA 1163
DB 671 AACCAATTGCAGACCAATTA 691
RESULT 10
FSOKCH
LOCUS
DEFINITION
Fusarium oxysporum k-family cellulase homologue mRNA, linear PLN 28-APR-1995
ACCESSION
L29381
VERSION
L29381.1 GI:520822
KEYWORDS
K-family cellulase homologue; cellulase; homologue.
SOURCE
Fusarium oxysporum cDNA to mRNA.
ORGANISM
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE
1 (bases 1 to 1443)
Sheppard,P.O., Grant,F.J., Oort,P.J., Oort,P.J., Sprecher,C.A., Foster,D.C.,
Hagen,F.S., Upshall,A., McKnight,G.L. and O'Hara,P.J.
The use of conserved cellulase family-specific sequences to clone
cellulase homologue cDNAs from Fusarium oxysporum
Gene 150 (1), 163-167 (1994)
95047531
PUBMED
7959045
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CKRDDSSFPAPKGTDSASKQPSAKKTTSAANAQPKTKDSAPVQKSTKPA
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BASE COUNT 325 a 448 c 332 g 338 t
ORIGIN
Query Match 15.0%; Score 221.4; DB 8; Length 1443;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
QY 547 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAGCTTCTTTCAGCTGGCCT 606
DB 137 TCTGAGCGGTCATCTTACTCGATCTGGGATTGCTGCAGCCCTTCTTCTTCTTGGAGC 196
QY 607 GGAAAGCTTCTGTCACTGGTCTCTGTGACACCTGTGCTGCCCTCCAATGGTATCTCTTTATTA 666

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Db      197  GGAAGGCTGCTGCAACGCCCTCTTAACCTTGTGATGAAGACGACAAACCCCATTTCC 256
QY      667  GATGCCAATGCTCAAAAGTGTTGTAA --- CGGTGGTAATGTTTCAATGTTGTAACAAAC 723
Db      257  AACACCAATGCTGTCAACGGTGTGAGGGTGTGTTCTGCTTATGCTTTCACCAACTAC 316
QY      724  CAACCTTGGGCTGTCAATGATGAGCTGCTTACGGTTCGCTGCTGCTCTATTGCTGGC 783
Db      317  TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTCGCTGCTCAACCAAGATCTCCGGT 376
QY      784  TCCACCAAGCTGATGAGTGTGTTGGCTGTATGAATGACCTTCACTTCTGCGCTGCT 843
Db      377  GGCTCCGAGCGCAGCTGTTGCTGTGCTGTGCTTACCTTCAACCTGCGCCCGTC 436
QY      844  TCTGGAAGAGATGTTGTTCAAGTTACCAACCGGTGGCGATTTAGGCTCTTAACCAAC 903
Db      437  AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACCAAC 496
QY      904  TTTGATTTGCAATGCCCGGTGGTGGTGTGATTTCAATGGCTGTGCTGCTCAATGG 963
Db      497  TTCGATCTCATGATGCCCGGTGGTGGTGTGATTTCAATGGCTGTGCTGCTCAATGG 556
QY      964  GCGCTCTCCCAATGATGCTGGGAGCTAGATATGTTGCTGCTGCTGCTGCTGCTGCT 1023
Db      557  GG-----CAAGGCTCTCGCGGTGCCAGTACGGCGGTATCTCTCCCGAAGCGAATG 610
QY      1024  GCGCTCTCTCTCTCTCTCAAGCTGTTGTAATGGAGATTTCACTGCTGCTGCTGCTG 1083
Db      611  GATAGCTACCCGAGCTTCTCAAGGACGGTGGCGATTCGCGATTCGAGTGTGCTGAGAAC 670
QY      1084  TCTGATACCTTACCAATGACCTTCAAGGAGTGTACCTGTGCC 1124
Db      671  GCCGACACCTGACTTCACTTTTGAGCAGGTTTCAGTGCCC 711

RESULT 11
LOCUS      A21795      1473 bp      mRNA      linear      PAT 20-SEP-1995
DEFINITION F. oxysporum mRNA for endonuclease component.
ACCESSION  A21795
VERSION     A21795.1 GI:1246874
KEYWORDS   Fusarium oxysporum.
SOURCE      Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 19.08; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.98; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
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Db      151  TCTGGAAGCGGTCACTTACTCGATCTGGATTGCTGCAAGCCTTCTTGCTTTGGAGC 210
QY      607  GGAAGAGCTTCTGCTCACTGGTCCCTGTTGACACCTGCTCCCAATGGTATGCTCTTTATTA 666
Db      211  GGAAGAGCTGCTGTCAACGCCCTCTTAACTTTGGTAAAGACGACAAACCCCATTTCC 270
QY      667  GATGCCAATGCTCAAAAGTGTGTAA --- CGGTGGTAATGTTTCAATGTTGTAACAAAC 723
Db      271  AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTTATGCTTTCGACCAACTAC 330
QY      724  CAACCTTGGGCTGTCAATGATGAGCTGCTTACGGTTCGCTGCTGCTCTTATTTCTGGC 783
Db      331  TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTCGCTGCTACCAAGATCTCCGGT 390
QY      784  TCCACCAAGCTGATGAGTGTGTTGGCTGTATGAATGACCTTCACTTCTGCGCTGCT 843
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QY      844  TCTGGAAGAGATGTTGTTCAAGTTACCAACCGGTGGCGATTTAGGCTCTTAACCAAC 903
Db      451  AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACCAAC 510
QY      904  TTTGATTTGCAATGCCCGGTGGTGGTGTGATTTCAATGGCTGTGCTGCTCAATGG 963
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QY      964  GCGCTCTCCCAATGATGCTGGGAGCTAGATATGTTGCTGCTGCTGCTGCTGCTGCTG 1023
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QY      1024  GCGCTCTCTCTCTCTCTCAAGCTGTTGTAATGGAGATTTCACTGCTGCTGCTGCTG 1083
Db      625  GATAGCTACCCGAGCTTCTCAAGGACGGTGGCGATTCGCGATTCGAGTGTGCTGAGAAC 684
QY      1084  TCTGATACCTTACCAATGACCTTCAAGGAGTGTACCTGTGCC 1124
Db      685  GCCGACACCTGACTTCACTTTTGAGCAGGTTTCAGTGCCC 725

RESULT 12
LOCUS      A23637      1473 bp      mRNA      linear      PAT 19-SEP-1995
DEFINITION F. oxysporum endoglucanase gene.
ACCESSION  A23637
VERSION     A23637.1 GI:832888
KEYWORDS   endoglucanase.
SOURCE      Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 1473)
            Convents, A.C., Busch, A. and Baek, A.C.
            Detergent compositions with high activity cellulase and softening
            clays
            Patent: EP 0495258-A 3 22-JUL-1992;
            THE FROCTER & GARDLE COMPANY
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    CKRDDSSFPFAFKVDTASAKFQPSAKKTTSAALAAQPKTKDSAPVQKSSTKPAA
    QPEPTKPADKPTDKPAATKPAATKVPQVKNPKTKTKVRGTRGSCPAKTDTAKA
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BASE COUNT      343 a  453 c  337 g  340 t
ORIGIN

Query Match      19.0%; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 547 TCTGGCAGTGTGTCACAACTCGTTATTTGGGATTTGTTAAAGCTTCTTTCGAGCTGGCCT 606
DB 151 TCTGGAAGCGGTCACTCTACTCGATCTGGATTTGCTGCAAGCTTCTTGTCTTTGGAGC 210
QY 607 GGAAGAGCTTCTGCTCACTGCTGCTTGTGACACCTGCTCCCAATGGTATCTCTTTATTA 666
DB 211 GGAAGAGCTGCTGCTCAACGCCCTCTTAACTTTGATAAGAACGACCAACCCATTTC 270
QY 667 GATGCCAATGCTCAAGTGGTTGTAA---CGGTGGTAAATGGTTTCATGTGTAAACAAC 723
DB 271 AACACCAATGCTGCTCAACGGTTGTGAGGGTGGTGGTTCGTCTTATGCTTGGCAACTAC 330
QY 724 CAACCTTGGGCTGTGTCATGATGAGCTGCTTACGGTTTCGCTGCTGCTCTTATTTGCTGGC 783
DB 331 TCTCCCTGGGCTGTGTCATGATGAGCTTGTCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390
QY 784 TCACAGGAGCTGGATGGTGTGCTGCTTATGATGACCTTCACTTCTGCGCTGCT 843
DB 391 GGTCTCGAGCCAGCTGGTGTGCTTATGCTTATGCTTACCTTACCACTGCGCCCGTC 450
QY 844 TCTGAAAGAGATGGTGTCTCAAGTTACCAACCGGTGGCGATTAGGCTCTAACCCAC 903
DB 451 AAGGCGAAGAGATGATGCTCCAGTCCACCAACATCGGAGGTGATCTCGCGCAACACCAC 510
QY 904 TTGATTTGCAATGCGCGGTGGTGGTGTGTTGTTGTTTCAATGGCTGTGCTCAATGG 963
DB 511 TTCGATCTCATGATCCCGCGGTGGTGGTGTGTTGCTTATGCTTACCTTACCACTGCGCTG 570
QY 964 GCGCTCCCAATGATGGCTGGGAGCTAGATGTTGGTGTGCTGCTCTCTCTGACTGT 1023
DB 571 GG-----CAAGGCTCTCGCGGTGGCCAGTACGGCGGTATCTCTCCGAAAGCGAATGT 624
QY 1024 GCCTCTCTTCTCTGCTCTTCAAGCTGGTGTGTAATGAGAGATTCAACTGGTTCAGAAAC 1083
DB 625 GATAGTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTGCTGCTGCTGAGAAC 684
QY 1084 TCTGATAACCTTACCATGACCTTCAAGGAAAGTTTACCTGTCC 1124
DB 685 GCGACAACTTCACTTCACTTTCAGCAGGTTCAGTGCCC 725

RESULT 13
A23646
LOCUS      1473 bp  mRNA  linear  PAT 23-FEB-1995
DEFINITION F. oxysporum endoglucanase gene.
ACCESSION  A23646
VERSION     A23646.1  GI:832892
KEYWORDS   Fusarium oxysporum.
SOURCE     Fusarium oxysporum
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 1473)
AUTHORS   Convents, A.C., Busch, A. and Baek, A.C.
TITLE     Detergent compositions with high activity cellulase and quaternary
            ammonium compounds
JOURNAL   Patent: EP 0495554-A 3 22-JUL-1992;
            THE PROCTER & GAMBLE COMPANY
FEATURES   Location/Qualifiers
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JOURNAL Patent: EP 0495257-A 3 22-JUL-1992;  
THE PROCTER & GAMBLE COMPANY

FEATURES  
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Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

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A23959

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

A23959

Endoglucanase gene.

A23959

A23959.1

GI:832900

1473 bp

DNA

linear

PAT 01-MAR-1995

SOURCE  
ORGANISM

Fusarium oxysporum.  
Fusarium oxysporum  
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Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum  
complex.

REFERENCE 1 (bases 1 to 1473)

AUTHORS McCornquodale, F. and Busch, A.

TITLE Dye transfer inhibiting compositions

JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;

THE PROCTER & GAMBLE COMPANY

FEATURES

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